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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/706,243A

DATE: 05/09/2002
TIME: 13:49:09

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\05092002\I706243A.raw

3 <110> APPLICANT: Cox III, George N.
4 Case, Casey Christopher
5 Eisenberg, Stephen P.
6 Jarvis, Eric E.
7 Spratt, Sharon K.
9 <120> TITLE OF INVENTION: REGULATION OF ENDOGENOUS GENE EXPRESSION IN CELLS
10 USING ZINC FINGER PROTEINS
12 <130> FILE REFERENCE: 8325-0002.10 / S2-US3
14 <140> CURRENT APPLICATION NUMBER: 09/706,243A
15 <141> CURRENT FILING DATE: 2000-11-03
17 <160> NUMBER OF SEQ ID NOS: 43
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 25
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence:exemplary motif
28 of C2H2 class of zinc finger proteins (ZFP)
30 <220> FEATURE:
31 <221> NAME/KEY: MOD_RES
32 <222> LOCATION: (2)..(3)
33 <223> OTHER INFORMATION: Xaa = any amino acid
35 <220> FEATURE:
36 <221> NAME/KEY: MOD_RES
37 <222> LOCATION: (4)..(5)
38 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent
40 <220> FEATURE:
41 <221> NAME/KEY: MOD_RES
42 <222> LOCATION: (7)..(18)
43 <223> OTHER INFORMATION: Xaa = any amino acid
45 <220> FEATURE:
46 <221> NAME/KEY: MOD_RES
47 <222> LOCATION: (20)..(22)
48 <223> OTHER INFORMATION: Xaa = any amino acid
50 <220> FEATURE:
51 <221> NAME/KEY: MOD_RES
52 <222> LOCATION: (23)..(24)
53 <223> OTHER INFORMATION: Xaa = any amino acid, may be present or absent
55 <400> SEQUENCE: 1
W--> 56 Cys Xaa Xaa Xaa Xaa Cys Xaa
57 1 5 10 15
W--> 59 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His

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60 20 25
61 <210> SEQ ID NO: 2
62 <211> LENGTH: 10
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial Sequence
66 <220> FEATURE:
67 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
68 with two overlapping D-able subsites
70 <220> FEATURE:
71 <221> NAME/KEY: modified_base
72 <222> LOCATION: (1)..(2)
73 <223> OTHER INFORMATION: n = g,a,c or t
75 <220> FEATURE:
76 <221> NAME/KEY: modified_base
77 <222> LOCATION: (5)
78 <223> OTHER INFORMATION: n = g,a,c or t
80 <220> FEATURE:
81 <221> NAME/KEY: modified_base
82 <222> LOCATION: (8)
83 <223> OTHER INFORMATION: n = g,a,c or t
85 <220> FEATURE:
86 <221> NAME/KEY: modified_base
87 <222> LOCATION: (9)
88 <223> OTHER INFORMATION: n = a,c or t; if g, then position 10 cannot be g
89 or t
91 <220> FEATURE:
92 <221> NAME/KEY: modified_base
93 <222> LOCATION: (10)
94 <223> OTHER INFORMATION: n = a or c; if g or t, then position 9 cannot be g
96 <400> SEQUENCE: 2
W--> 97 nngkngknnn 10
100 <210> SEQ ID NO: 3
101 <211> LENGTH: 10
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
107 with three overlapping D-able subsites
109 <220> FEATURE:
110 <221> NAME/KEY: modified_base
111 <222> LOCATION: (1)..(2)
112 <223> OTHER INFORMATION: n = g,a,c or t
114 <220> FEATURE:
115 <221> NAME/KEY: modified_base
116 <222> LOCATION: (5)
117 <223> OTHER INFORMATION: n = g,a,c or t
120 <220> FEATURE:
121 <221> NAME/KEY: modified_base
122 <222> LOCATION: (8)

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123 <223> OTHER INFORMATION: n = g,a,c or t
125 <400> SEQUENCE: 3
W--> 126 nngkngkngk 10
129 <210> SEQ ID NO: 4
130 <211> LENGTH: 5
131 <212> TYPE: PRT
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
137 <400> SEQUENCE: 4
138 Asp Gly Gly Gly Ser
139 1 5
142 <210> SEQ ID NO: 5
143 <211> LENGTH: 5
144 <212> TYPE: PRT
145 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
150 <400> SEQUENCE: 5
151 Thr Gly Glu Lys Pro
152 1 5
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 9
157 <212> TYPE: PRT
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
163 <400> SEQUENCE: 6
164 Leu Arg Gln Lys Asp Gly Glu Arg Pro
165 1 5
168 <210> SEQ ID NO: 7
169 <211> LENGTH: 4
170 <212> TYPE: PRT
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
176 <400> SEQUENCE: 7
177 Gly Gly Arg Arg
178 1
181 <210> SEQ ID NO: 8
182 <211> LENGTH: 5
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
189 <400> SEQUENCE: 8
190 Gly Gly Gly Gly Ser
191 1 5
194 <210> SEQ ID NO: 9

RAW SEQUENCE LISTING DATE: 05/09/2002
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195 <211> LENGTH: 8
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
202 <400> SEQUENCE: 9
203 Gly Gly Arg Arg Gly Gly Gly Ser
204 1 5
207 <210> SEQ ID NO: 10
208 <211> LENGTH: 9
209 <212> TYPE: PRT
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
215 <400> SEQUENCE: 10
216 Leu Arg Gln Arg Asp Gly Glu Arg Pro
217 1 5
220 <210> SEQ ID NO: 11
221 <211> LENGTH: 12
222 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
228 <400> SEQUENCE: 11
229 Leu Arg Gln Lys Asp Gly Gly Ser Glu Arg Pro
230 1 5 10
233 <210> SEQ ID NO: 12
234 <211> LENGTH: 16
235 <212> TYPE: PRT
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence:linker
242 <400> SEQUENCE: 12
243 Leu Arg Gln Lys Asp Gly Gly Ser Gly Gly Ser Glu Arg Pro
244 1 5 10 15
247 <210> SEQ ID NO: 13
248 <211> LENGTH: 25
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence:ZFP target site
254 region surrounding initiation site of vascular
255 endothelial growth factor (VEGF) gene containing
256 two 9-base pair target sites
258 <220> FEATURE:
259 <221> NAME/KEY: protein_bind
260 <222> LOCATION: (4)..(12)
261 <223> OTHER INFORMATION: upstream 9-base pair ZFP VEGF1 target site
263 <220> FEATURE:

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264 <221> NAME/KEY: protein_bind
 265 <222> LOCATION: (14)..(22)
 266 <223> OTHER INFORMATION: downstream 9-base pair ZFP VEGF3a target site
 268 <400> SEQUENCE: 13
 269 agcgccccagg atcgccggagg cttgg 25
 272 <210> SEQ ID NO: 14
 273 <211> LENGTH: 298
 274 <212> TYPE: DNA
 275 <213> ORGANISM: Artificial Sequence
 277 <220> FEATURE:
 278 <223> OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
 279 construct targeting upstream 9-base pair target
 280 site in VEGF promoter
 282 <220> FEATURE:
 283 <221> NAME/KEY: CDS
 284 <222> LOCATION: (2)..(298)
 285 <223> OTHER INFORMATION: VEGF1
 287 <400> SEQUENCE: 14
 288 g gta ccc ata cct ggc aag aag aag cag cac atc tgc cac atc cag ggc 49
 289 Val Pro Ile Pro Gly Lys Lys Gln His Ile Cys His Ile Gln Gly
 290 1 5 10 15
 292 tgt ggt aaa gtt tac ggc aca acc tca aat ctg cgt cgt cac ctg cgc 97
 293 Cys Gly Lys Val Tyr Gly Thr Ser Asn Leu Arg Arg His Leu Arg
 294 20 25 30
 296 tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt 145
 297 Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
 298 35 40 45
 300 aaa cgc ttc acc cgt tcg tca aac ctg cag cgt cac aag cgt acc cac 193
 301 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
 302 50 55 60
 303 acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg 241
 304 Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
 305 65 70 75 80
 307 cgt agt gac cac ctg tcc cgt cac atc aag acc cac cag aat aag aag 289
 308 Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
 309 85 90 95
 311 ggt gga tcc 298
 312 Gly Gly Ser
 315 <210> SEQ ID NO: 15
 316 <211> LENGTH: 99
 317 <212> TYPE: PRT
 318 <213> ORGANISM: Artificial Sequence
 320 <220> FEATURE:
 321 <223> OTHER INFORMATION: Description of Artificial Sequence:VEGF1 ZFP
 322 construct targeting upstream 9-base pair target
 323 site in VEGF promoter
 325 <400> SEQUENCE: 15
 326 Val Pro Ile Pro Gly Lys Lys Gln His Ile Cys His Ile Gln Gly
 327 1 5 10 15

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/09/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24
Seq#:2; N Pos. 1,2,5,8,9,10
Seq#:3; N Pos. 1,2,5,8
Seq#:41; N Pos. 1,2
Seq#:42; N Pos. 1,2
Seq#:43; N Pos. 1,2

VARIABLE LOCATION, SUMMARY DATE: 05/09/2002
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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is **MANDATORY** if n's or xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:1; Xaa Pos. 2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24
Seq#:2; N Pos. 1,2,5,8,9,10
Seq#:3; N Pos. 1,2,5,8
Seq#:41; N Pos. 1,2
Seq#:42; N Pos. 1,2
Seq#:43; N Pos. 1,2

VERIFICATION SUMMARY

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L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:861 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:41
L:861 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:41
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:873 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:42
L:873 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:42
L:873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:885 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:885 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0